**GWAS summary statistics of psoriasis**

General information:

* **Sample size**: 1,415 psoriasis cases and 3,968 control participants
* **Sequencing platform**: Illumina HiSeq X Ten or NovaSeq 6000
* **Sample QC**: We excluded samples with (i) excessive heterozygosity (het/hom ratio >0.365), (ii) a low genotype call rate (<0.95), (iii) aberrantly high or low Ti/Tv ratio, (iv) closely related individuals (KING kingship coefficient cutoff > 0.0884), and (v) non-East Asian ancestry based on PCA.
* **Variant QC**: We excluded the variant sites (i) located in the low complexity regions, (ii) with Hardy–Weinberg *P* value <1.0 × 10−10, (iii) with more than three alleles, (iv) with indels larger than 100bp, (v) with spanning deletions, or (vi) with genotyping call rate <0.95. In addition, we removed variants showing a significant difference in allele frequency (*χ*2 >300) compared with reference datasets of Japanese ancestry.
* **Association test**: We statistically tested the association of common genetic variants (minor allele frequency >0.5%) with the psoriasis risk using a logistic regression assuming an additive genetic model as implemented in PLINK2 version 2.00a3LM with the adjustment of the top 10 PCs. Association test results were produced separately for the two sequencing platforms and subsequently meta-analyzed using the inverse-variance weighted fixed effect model implemented in METAL (version 2011-03-25).

Uploaded file

| **File name** | **Descriptions** |
| --- | --- |
| GWASsummary\_PsV\_Japanese\_SoneharaCellGenomics2025.txt.gz | Results for 8,209,780 variants |

Columns

| **#** | **column name** | **descriptions** |
| --- | --- | --- |
| 1 | MarkerName | marker name (CHR:POS\_REF/ALT in GRCh37) |
| 2 | Allele1 | non-effect allele |
| 3 | Allele2 | effect allele |
| 4 | Freq | allele frequency of the effect allele |
| 5 | Effect | effect size of the effect allele |
| 6 | StdErr | standard error of Effect |
| 7 | P-value | *P*-value for Effect |
| 8 | Direction | summary of effect direction for each study |
| 9 | HetISq | *I*2 statistic representing the between-study heterogeneity |
| 10 | HetChiSq | *χ*2 statistic representing the between-study heterogeneity |
| 11 | HetDf | degrees of freedom for heterogeneity statistic |
| 12 | HetPVal | *P*-value for heterogeneity statistic |

Reference

If you use the summary statistics, please cite the following paper:  
Sonehara K et al. Whole-genome sequencing reveals rare and structural variants contributing to psoriasis and identifies *CERCAM* as a risk gene. *Cell Genomics* 2025.